

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: WALLACH, David
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METT, Igor
ENGELMANN, Hartmut
- (ii) TITLE OF INVENTION: TNF INHIBITORS
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
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(C) CITY: Washington
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(E) COUNTRY: USA
(F) ZIP: 20004
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/476,862
(B) FILING DATE: 07-JUN-1995
(C) CLASSIFICATION: 514
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: IL 107267
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- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: IL 94039
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- (vii) PRIOR APPLICATION DATA:
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(B) FILING DATE: 06-AUG-1989
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: IL 90339
(B) FILING DATE: 18-MAY-1989
- (viii) ATTORNEY/AGENT INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 90..1472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCGAGCGCAG CGGAGCCTGG AGAGAAGGCG CTGGGCTGCG AGGGCGCGAG GGCGCGAGGG	60
CAGGGGGCAA CCGGACCCCG CCCGCACCC ATG GCG CCC GTC GCC GTC TGG GCC	113
Met Ala Pro Val Ala Val Trp Ala	
1 5	
GCG CTG GCC GTC GGA CTG GAG CTC TGG GCT GCG GCG CAC GCC TTG CCC	161
Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala Ala His Ala Leu Pro	
10 15 20	
GCC CAG GTG GCA TTT ACA CCC TAC GCC CCG GAG CCC GGG AGC ACA TGC	209
Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys	
25 30 35 40	
CGG CTC AGA GAA TAC TAT GAC CAG ACA GCT CAG ATG TGC TGC AGC AAA	257
Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys	
45 50 55	
TGC TCG CCG GGC CAA CAT GCA AAA GTC TTC TGT ACC AAG ACC TCG GAC	305
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp	
60 65 70	
ACC GTG TGT GAC TCC TGT GAG GAC AGC ACA TAC ACC CAG CTC TGG AAC	353
Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn	
75 80 85	
TGG GTT CCC GAG TGC TTG AGC TGT GGC TCC CGC TGT AGC TCT GAC CAG	401
Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln	
90 95 100	
GTG GAA ACT CAA GCC TGC ACT CGG GAA CAG AAC CGC ATC TGC ACC TGC	449
Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys	
105 110 115 120	
AGG CCC GGC TGG TAC TGC GCG CTG AGC AAG CAG GAG GGG TGC CGG CTG	497
Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg Leu	
125 130 135	
TGC GCG CCG CTG CGC AAG TGC CGC CCG GGC TTC GGC GTG GCC AGA CCA	545
Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg Pro	
140 145 150	
GGA ACT GAA ACA TCA GAC GTG GTG TGC AAG CCC TGT GCC CCG GGG ACG	593
Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr	
155 160 165	
TTC TCC AAC ACG ACT TCA TCC ACG GAT ATT TGC AGG CCC CAC CAG ATC	641
Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile	
170 175 180	
TGT AAC GTG GTG GCC ATC CCT GGG AAT GCA AGC ATG GAT GCA GTC TGC	689
Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys	
185 190 195 200	
ACG TCC ACG TCC CCC ACC CGG AGT ATG GCC CCA GGG GCA GTA CAC TTA	737
Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val His Leu	
205 210 215	

CCC Pro	CAG Gln	CCA Pro	GTG Val 220	TCC Ser	ACA Thr	CGA Arg	TCC Ser	CAA Gln 225	CAC His	ACG Thr	CAG Gln	CCA Pro	ACT Thr 230	CCA Pro	GAA Glu	785											
CCC Pro	AGC Ser	ACT Thr 235	GCT Ala	CCA Pro	AGC Ser	ACC Thr	TCC Ser 240	TTC Phe	CTG Leu	CTC Leu	CCA Pro	ATG Met 245	GGC Gly	CCC Pro	AGC Ser	833											
CCC Pro	CCA Pro 250	GCT Ala	GAA Glu	GGG Gly	AGC Ser	ACT Thr 255	GGC Gly	GAC Asp	TTC Phe	GCT Ala	CTT Leu 260	CCA Pro	GTT Val	GGA Gly	CTG Leu	881											
ATT Ile 265	GTG Val	GGT Gly	GTG Val	ACA Thr 270	GCC Ala	TTG Leu	GGT Gly	CTA Leu	CTA Leu	ATA Ile 275	ATA Ile	GGA Gly	GTG Val	GTG Val	AAC Asn 280	929											
TGT Cys	GTC Val	ATC Ile	ATG Met	ACC Thr 285	CAG Gln	GTG Val	AAA Lys	AAG Lys	AAG Lys	CCC Pro	TTG Leu	TGC Cys	CTG Leu	CAG Gln 295	AGA Arg	977											
GAA Glu	GCC Ala	AAG Lys	GTG Val 300	CCT Pro	CAC His	TTG Leu	CCT Pro	GCC Ala 305	GAT Asp	AAG Lys	GCC Ala	CGG Arg	GGT Gly 310	ACA Thr	CAG Gln	1025											
GGC Gly	CCC Pro	GAG Glu 315	CAG Gln	CAG Gln	CAC His	CTG Leu	CTG Leu 320	ATC Ile	ACA Thr	GCG Ala	CCG Pro	AGC Ser 325	TCC Ser	AGC Ser	AGC Ser	1073											
AGC Ser 330	TCC Ser	CTG Leu	GAG Glu	AGC Ser	TCG Ser	GCC Ala 335	AGT Ser	GCG Ala	TTG Leu	GAC Asp	AGA Arg 340	AGG Arg	GCG Ala	CCC Pro	ACT Thr	1121											
CGG Arg 345	AAC Asn	CAG Gln	CCA Pro	CAG Gln	GCA Ala 350	CCA Pro	GGC Gly	GTG Val	GAG Glu	GCC Ala 355	AGT Ser	GGG Gly	GCC Ala	GGG Gly	GAG Glu 360	1169											
GCC Ala	CGG Arg	GCC Ala	AGC Ser	ACC Thr 365	GGG Gly	AGC Ser	TCA Ser	GAT Asp	TCT Ser 370	TCC Ser	CCT Pro	GGT Gly	GGC Gly	CAT His 375	GGG Gly	1217											
ACC Thr	CAG Gln	GTC Val 380	AAT Asn	GTC Val	ACC Thr	TGC Cys	ATC Ile	GTG Val 385	AAC Asn	GTC Val	TGT Cys	AGC Ser	AGC Ser	TCT Ser	GAC Asp	1265											
CAC His	AGC Ser	TCA Ser 395	CAG Gln	TGC Cys	TCC Ser	TCC Ser	CAA Gln 400	GCC Ala	AGC Ser	TCC Ser	ACA Thr	ATG Met 405	GGA Gly	GAC Asp	ACA Thr	1313											
GAT Asp 410	TCC Ser	AGC Ser	CCC Pro	TCG Ser	GAG Glu	TCC Ser 415	CCG Pro	AAG Lys	GAC Asp	GAG Glu	CAG Gln 420	GTC Val	CCC Pro	TTC Phe	TCC Ser	1361											
AAG Lys 425	GAG Glu	GAA Glu	TGT Cys	GCC Ala	TTT Phe 430	CGG Arg	TCA Ser	CAG Gln	CTG Leu	GAG Glu 435	ACG Thr	CCA Pro	GAG Glu	ACC Thr	CTG Leu 440	1409											
CTG Leu	GGG Gly	AGC Ser	ACC Thr	GAA Glu 445	GAG Glu	AAG Lys	CCC Pro	CTG Leu	CCC Pro	CTT Leu	GGA Gly	GTG Val	CCT Pro	GAT Asp 455	GCT Ala	1457											
GGG Gly	ATG Met	AAG Lys	CCC Pro 460	AGT Ser	TAACCAGGCC GGTGTGGGCT GTGTCGTAGC CAAGGTGGGC											1512											
TGAGCCCTGG CAGGATGACC CTGCGAAGGG GCCCTGGTCC TTCCAGGCCC CCACCACTAG																1572											
GACTCTGAGG CTCTTTCTGG GCCAAGTTCC TCTAGTGCCC TCCACAGCCG CAGCCTCCCT																1632											

CTGACCTGCA GGCCAAGAGC AGAGGCAGCG AGTTGGGGAA AGCCTCTGCT GCCATGGTGT 1692
 GTCCCTCTCG GAAGGCTGGC TGGGCATGGA CGTTCGGGGC ATGCTGGGGC AAGTCCCTGA 1752
 CTCTCTGTGA CCTGCCCCGC CCAGCTGCAC CTGCCAGCCT GGCTTCTGGA GCCCTTGGGT 1812
 TTTTGTGTTG TTTGTTTGTG TGTGTTGTTG TTTCTCCCCC TGGGCTCTGC CCAGCTCTGG 1872
 CTTCAGAAAA ACCCCAGCAT CCTTTTCTGC AGAGGGGCTT TCTGGAGAGG AGGGATGCTG 1932
 CCTGAGTCAC CCATGAAGAC AGGACAGTGC TTCAGCCTGA GGCTGAGACT GCGGGATGGT 1992
 CCTGGGGCTC TGTGTAGGGA GGAGGTGGCA GCCCTGTAGG GAACGGGGTC CTTCAAGTTA 2052
 GCTCAGGAGG CTTGGAAGC ATCACCTCAG GCCAGGTGCA GTGGCTCACG CCTATGATCC 2112
 CAGCACTTTG GGAGGCTGAG GCGGGTGGAT CACCTGAGGT TAGGAGTTCG AGACCAGCCT 2172
 GGCCAACATG GTAAAACCCC ATCTCTACTA AAAATACAGA AATTAGCCGG GC 2224

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
 1 5 10 15
 Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
 20 25 30
 Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
 35 40 45
 Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
 50 55 60
 Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
 65 70 75 80
 Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
 85 90 95
 Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
 100 105 110
 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
 115 120 125
 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
 130 135 140
 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 145 150 155 160
 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
 165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
 180 185 190
 Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 195 200 205
 Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
 210 215 220
 Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
 225 230 235 240
 Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
 245 250 255
 Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
 260 265 270
 Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
 275 280 285
 Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
 290 295 300
 Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
 305 310 315 320
 Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
 325 330 335
 Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
 340 345 350
 Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
 355 360 365
 Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
 370 375 380
 Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
 385 390 395 400
 Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
 405 410 415
 Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
 420 425 430
 Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
 435 440 445
 Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
 450 455 460

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 153 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys
 1 5 10 15
 Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly
 20 25 30
 Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr
 35 40 45
 Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg
 50 55 60
 Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp
 65 70 75 80
 Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu
 85 90 95
 Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val
 100 105 110
 His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala
 115 120 125
 Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys
 130 135 140
 Lys Ser Leu Glu Cys Thr Lys Leu Cys
 145 150

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 163 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys
 1 5 10 15
 Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr
 20 25 30
 Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
 35 40 45
 Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Asp
 50 55 60
 Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
 65 70 75 80
 Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
 85 90 95
 Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala
 100 105 110
 Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro
 115 120 125

Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His
 130 135 140
 Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala
 145 150 155 160
 Val Cys Thr

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gln Asn Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro
 1 5 10 15
 Cys Pro Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp
 20 25 30
 Glu Pro Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys
 35 40 45
 Ala His Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly
 50 55 60
 His Gly Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys
 65 70 75 80
 Cys Arg Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His
 85 90 95
 Cys Asp Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr
 100 105 110
 Leu Thr Ser Asn Thr Lys Cys
 115

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 159 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Cys Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala
 1 5 10 15
 Cys Asn Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr
 20 25 30
 Val Cys Glu Pro Cys Leu Asp Ser Val Thr Ser Ser Asp Val Val Ser
 35 40 45

Ala Thr Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser
50 55 60
His Ser Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala
65 70 75 80
Tyr Gly Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg
85 90 95
Val Cys Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln
100 105 110
Asn Thr Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala
115 120 125
Asn His Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu
130 135 140
Arg Gln Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu
145 150 155

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Cys Arg Glu Lys Gln Tyr Leu Ile Asn Ser Gln Cys Cys Ser Leu
1 5 10 15
Cys Gln Pro Gly Gln Lys Leu Val Ser Asp Cys Thr Glu Phe Thr Glu
20 25 30
Thr Glu Cys Leu Pro Cys Gly Glu Ser Glu Phe Leu Asp Thr Trp Asn
35 40 45
Arg Glu Thr His Cys His Gln His Lys Tyr Cys Asp Pro Asn Leu Gly
50 55 60
Leu Arg Val Gln Gln Lys Gly Thr Ser Glu Thr Asp Thr Ile Cys Thr
65 70 75 80
Cys Glu Glu Gly Trp His Cys Thr Ser Glu Ala Cys Glu Ser Cys Val
85 90 95
Leu His Arg Ser Cys Ser Pro Gly Phe Gly Val Lys Gln Ile Ala Thr
100 105 110
Gly Val Ser Asp Thr Ile Cys Glu Pro Cys Pro Val Gly Phe Phe Ser
115 120 125
Asn Val Ser Ser Ala Phe Glu Lys Cys His Pro Thr Ser Cys Glu Thr
130 135 140
Lys Asp Leu Val Val Gln Gln Ala Gly Thr Asn Lys Thr Asp Val Val
145 150 155 160
Cys Gly

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asn	Cys	Val	Lys	Asp	Thr	Tyr	Pro	Ser	Gly	His	Lys	Cys	Cys	Arg	Glu
1			5						10					15	
Cys	Gln	Pro	Gly	His	Gly	Met	Val	Ser	Arg	Cys	Asp	His	Thr	Arg	Asp
			20					25					30		
Thr	Val	Cys	His	Pro	Cys	Glu	Pro	Gly	Phe	Tyr	Asn	Glu	Ala	Val	Asn
		35					40					45			
Tyr	Asp	Thr	Cys	Lys	Gln	Cys	Thr	Gln	Cys	Asn	His	Arg	Ser	Gly	Ser
	50					55					60				
Glu	Leu	Lys	Gln	Asn	Cys	Thr	Pro	Thr	Glu	Asp	Thr	Val	Cys	Gln	Cys
65					70					75					80
Arg	Pro	Gly	Thr	Gln	Pro	Arg	Gln	Asp	Ser	Ser	His	Lys	Leu	Gly	Val
				85					90					95	
Asp	Cys	Val	Pro	Cys	Pro	Pro	Gly	His	Phe	Ser	Pro	Gly	Ser	Asn	Gln
			100					105					110		
Ala	Cys	Lys	Pro	Trp	Thr	Asn	Cys	Thr	Leu	Ser	Gly	Lys	Gln	Ile	Arg
		115					120					125			
His	Pro	Ala	Ser	Asn	Ser	Leu	Asp	Thr	Val	Cys	Glu				
	130					135					140				